

(v) identifying, isolating and characterizing genes the transcription of which was enhanced by said element which functions to enhance gene expression.

2. (Twice Amended) The method of claim 1, further comprising the steps of  
(vi) preparing a separate heterologous gene construct for each isolated gene;  
(vii) transforming plants with said separate heterologous gene construct wherein expression of the isolated gene is enhanced in said plants;  
(viii) selecting plants having the desired trait.

3. (Amended) The method of claim 1, wherein the enhancer is selected from the group consisting of a CaMV35S enhancer element, a Figwort Mosaic Virus (FMV) promoter, a Figwort Mosaic Virus (FMV) enhancer, a peanut chlorotic streak caulimovirus full-length transcript (PCISVFLt) sequence, a mirabilis mosaic virus (MMV) promoter and a mirabilis mosaic virus (MMV) enhancer.

4. (Twice amended) The method of claim 3, wherein said enhancer is the CaMV35S enhancer element, and wherein the CaMV35S enhancer element is a 4X tandem duplicated CaMV35S enhancer element having the sequence presented as SEQ ID NO:1.

5. (Twice amended) The method of claim 3, wherein said enhancer is the Figwort Mosaic Virus (FMV) promoter having the sequence presented as SEQ ID NO:5 or the Figwort Mosaic Virus (FMV) enhancer having the sequence presented as SEQ ID NO:6.

6. (Twice amended) The method of claim 3, wherein said enhancer is the peanut chlorotic streak caulimovirus full-length transcript (PCISVFLt) sequence, and wherein the PCISVFLt sequence is the enhancer having the sequence presented as SEQ ID NO:7.

7. (Twice amended) The method of claim 3, wherein said enhancer is the mirabilis mosaic virus (MMV) promoter having the sequence presented as SEQ ID NO:8 or the mirabilis mosaic virus (MMV) enhancer having the sequence presented as nucleotides 1-260 of SEQ ID NO:8.

11. (Amended) The method of claim 1, wherein said fleshy fruit-bearing plant is a dwarf plant.

19. (Amended) A transgenic fleshy fruit-bearing plant comprising enhanced expression of a gene identified by the method of claim 1, wherein the gene is associated with a morphological characteristic selected from the group consisting of leaflet size, leaf size, leaf color, leaf shape, leaflet number, leaf number, internode length, plant height, floral organ characteristics and fruit characteristics.

Please add new claims 20 – 23 as follows:

20. (New) A method for identifying genes associated with a desired trait in a tomato plant comprising: